

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 12, 2002, 20:42:35 ; Search time 23.96 seconds
(without alignments)
325.944 Million cell updates/sec

Title: US-09-525-867-1

Perfect score: 1118

Sequence: 1 MAVLSAPGLRGFRILGRSS.....ILOLQRIKRRRLQIWR 213

Scoring table:

BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1108	99.1	213	1	NUKM_HUMAN
2	965.5	86.4	216	1	NUKM_BOVIN
3	736	65.8	215	1	NUKM_BRAOL
4	732.5	65.5	213	1	NUKM_SOLTU
5	726.5	65.0	199	1	NUKM_CABEL
6	725	64.8	218	1	NUKM_ARATH
7	719.5	64.4	226	1	NUKM_NEUCR
8	718	64.2	182	1	NUKM_RECAM
9	654.5	58.5	174	1	NUOB_RICPR
10	643	57.5	177	1	NUOB_RHOCA
11	639	57.2	192	1	NUBL_RHIME
12	626	56.0	173	1	NUOB_PARDE
13	561	50.2	156	1	NUKM_PARTE
14	521	46.6	179	1	NUOB_AQUAE
15	519	46.4	202	1	NUKM_TRYBB
16	502.5	44.9	167	1	NUB2_RHIME
17	457	40.9	181	1	NUOB_RHETH
18	444	39.7	220	1	NUOB_ECOLI
19	440.5	39.4	247	1	NUKM_MESVI
20	438	39.2	248	1	NUKC_SYNV3
21	437.5	39.1	184	1	NUOB_MYCTU
22	431.5	38.6	225	1	NUKC_ARATH
23	431.5	38.6	247	1	NUKC_TOBAC
24	429.5	38.4	244	1	NUKC_SPTOL
25	429.5	38.4	245	1	NUKM_ANASQ
26	428	38.3	224	1	NUOB_BUCAI
27	427.5	38.2	246	1	NUKC_ORYSA
28	426.5	38.1	243	1	NUKC_MARPO
29	424.5	38.0	219	1	NUKC_SYNV3
30	424	37.9	224	1	NUOB_ERWCA
31	423.5	37.9	226	1	NUKC_LUPLU
32	423.5	37.9	245	1	NUKC_WHEAT
33	422.5	37.8	248	1	NUKC_MAIZE

34	420.5	37.6	245	1	NUKC_ANASP
35	408.5	36.5	224	1	NUKC_SOIBN
36	275	24.6	255	1	HYCG_ECOLI
37	255	22.8	252	1	HYFL_ECOLI
38	131	11.7	80	1	NUKC_ANTFO
39	104	9.3	230	1	FRHG_METJA
40	97.5	8.7	235	1	FRHG_METTH
41	97	8.7	216	1	Y736_METJA
42	92.5	8.3	1239	1	V120_EBV
43	88.5	7.9	510	1	PNTA_ECOLI
44	82	7.3	243	1	FRHG_METVO
45	80	7.2	209	1	HOXY_ALCEU

ALIGNMENTS

RESULT 1
ID NUKM_HUMAN STANDARD; PRT; 213 AA.
AC 075251;
DT 15-JUL-1999 (Rel. 38, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT, MITOCHONDRIAL PRECURSOR
(EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT).
GN NDUFS7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE=97092888; PubMed=8938450;
RA Hyslop S.J., Duncan A.M., Pitkanen S., Robinson B.H.;
RT "Assignment of the PSST subunit gene of human mitochondrial complex I
to chromosome 19p13.";
RL Genomics 37:375-380(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97092888; PubMed=8938450;
RA Hyslop S.J., Duncan A.M., Pitkanen S., Robinson B.H.;
RT "Assignment of the PSST subunit gene of human mitochondrial complex I
to chromosome 19p13.";
RL Genomics 37:375-380(1996).
RN [2]
RP SEQUENCE OF 56-213 FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Carnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Krommiller B., Arriano A., Montgomey M., Ow D., Nolan M., Trong S.,
Kobayashi A., Olsen A.S., Carrano A.V.;
RA Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[3]
RP VARIANT LS MET-122.
RX MEDLINE=99287516; PubMed=10360771;
RA Triepels R.H., van den Heuvel L., Loeffen J.L., Buskens C.A.,
Smeets R.J., Rubio Gozalbo M.E., Budde S.M., Mariman E.C.,
Wijburg F.A., Barth P.G., Trijbels J.M.F., Smeitink J.A.;
RA "Leigh syndrome associated with a mutation in the NDUFS7 (PSST)
nuclear encoded subunit of complex I";
RL Ann. Neurol. 45:787-790(1999)
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
CC -1- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
CC -1- DISEASE: DEFECTS IN NDUFS7 ARE A CAUSE OF LEIGH SYNDROME (LS); A
SEVERE NEUROLOGICAL DISORDER CHARACTERIZED BY BILATERALLY
SYMMETRICAL NECROTIC LESIONS IN SUBCORTICAL BRAIN REGIONS.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 20 KDA SUBUNIT FAMILY.
CC
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EMBL: AC005329; AAC27669.1; -
 DR MM: 601825; -
 DR MM: 256000; -
 DR InterPro: IPR002096; Complex1_20kD.
 DR Pfam: PF01058; oxidored_g6; 2.
 DR PROSITE: PS01150; COMPLEX1_20K; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;
 FT Iron-sulfur; 4Fe-4S; Disease mutation; Leigh syndrome.
 FT TRANSIT 1 38 MITOCHONDRION (BY SIMILARITY).
 FT CHAIN 39 213 NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA
 SUBUNIT.
 FT METAL 88 88 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 89 89 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 153 153 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 183 183 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT VARIANT 122 122 V->M (IN LS).
 FT /FTD=VAR_008848.
 SQ SEQUENCE 213 AA: 23579 MW; B863199E06538DEC CRC64;

Query Match 99.1%; Score 1108; DB 1; Length 213;
 Best Local Similarity 99.5%; Pred. No. 2.8e-99;
 Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAVLSAPGLRGFRILGLRSSVGPVAVQARGVHQSVDTPGSPSTQPALPKARAVAPKPSRRG 60
 DB 1 MAVLSAPGLRGFRILGLRSSVGPVAVQARGVHQSVDTPGSPSTQPALPKARAVAPKPSRRG 60
 QY 61 EYVAKLDLVNARRSSLPWTFGLACCAVEMHMAAPRYDMDRFGVFRASPRQSDVM 120
 DB 61 EYVAKLDLVNARRSSLPWTFGLACCAVEMHMAAPRYDMDRFGVFRASPRQSDVM 120
 QY 121 IVAGILTNKMAPALRKRYDQMPPEPRYVYVSMGSCANGGYYHYSYVVGCDRIVPVDIYI 180
 DB 121 IVAGILTNKMAPALRKRYDQMPPEPRYVYVSMGSCANGGYYHYSYVVGCDRIVPVDIYI 180
 QY 181 PGCPTAEALLYGILQLOKRIKRRRLQIWR 213
 DB 181 PGCPTAEALLYGILQLOKRIKRRRLQIWR 213

RESULT 2
 NUKM_BOVIN
 ID NUKM_BOVIN STANDARD; PRT; 216 AA.
 AC P42026;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT, MITOCHONDRIAL PRECURSOR
 DE (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT).
 GN NDUF57.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=9249573; PubMed=1577158;
 RA Arizemendi J.M., Runswick M.J., Skehel J.M., Walker J.E.;
 RT "NADH: ubiquinone oxidoreductase from bovine heart mitochondria. A
 fourth nuclear encoded subunit with a homologue encoded in
 Chloroplast genomes";
 RL FEBS Lett. 301:237-242 (1992).
 CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
 CC -|- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
 CC -|- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
 CC -|- SIMILARITY: BELONGS TO THE COMPLEX I 20 KDA SUBUNIT FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
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EMBL: X65020; CAA46154.1; -
 DR InterPro: IPR002096; Complex1_20kD.
 DR Pfam: PF01058; oxidored_g6; 1.
 DR PROSITE: PS01150; COMPLEX1_20K; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;
 FT Iron-sulfur; 4Fe-4S; 37
 FT CHAIN 38 216 NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA
 SUBUNIT.
 FT METAL 91 91 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 92 92 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 156 156 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 186 186 IRON-SULFUR (4FE-4S) (POTENTIAL).
 SQ SEQUENCE 216 AA: 23771 MW; 514B8A63C59BE641 CRC64;

Query Match 86.4%; Score 965.5; DB 1; Length 216;
 Best Local Similarity 85.7%; Pred. No. 1.4e-85;
 Matches 186; Conservative 11; Mismatches 15; Indels 5; Gaps 2;

QY 1 MAVLSAPGLRGFRILGLRSSVGPVAVQARGVHQSVDTPGSPSTQPALPKARAVAPKPSRRG 56
 DB 1 MAALAARLL-L-HPILAVRSGVGAALQVRGVHSSMAADSPSTQPAVSQARAVVPKPAALP 59
 QY 57 SSRGEYVYVAKLDLVNARRSSLPWTFGLACCAVEMHMAAPRYDMDRFGVFRASPRQ 116
 DB 60 SSRGEYVYVAKLDLVNARRSSLPWTFGLACCAVEMHMAAPRYDMDRFGVFRASPRQ 119
 QY 117 SDVMIVAGTLTNKMAPALRKRYDQMPPEPRYVYVSMGSCANGGYYHYSYVVGCDRIVP 176
 DB 120 SDVMIVAGTLTNKMAPALRKRYDQMPPEPRYVYVSMGSCANGGYYHYSYVVGCDRIVP 179
 QY 177 DIVPGCPPTAEALLYGILQLOKRIKRRRLQIWR 213
 DB 180 DIVPGCPPTAEALLYGILQLOKRIKRRRLQIWR 216

RESULT 3
 NUKM_BRAOL
 ID NUKM_BRAOL STANDARD; PRT; 215 AA.
 AC P42027;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE 20 KDA SUBUNIT, MITOCHONDRIAL PRECURSOR
 DE (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-20KD) (CI-20KD).
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OC NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SHOGUN; TISSUE=Fluores;.
 RX MEDLINE=95334517; PubMed=7610188;
 RA Pogson B.J., Downs C.G., Davies K.M., Morris S.C.,
 RA Buchanan-Wollaston V.;
 RT "Nucleotide sequence of a cDNA clone from broccoli with high identity
 with the PSST subunit of NADH:ubiquinone oxidoreductase";
 RL Plant Physiol. 108:859-860 (1995).
 CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE -> NAD(+) + UBIQUINOL.
 CC -|- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
 CC -|- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
 CC -|- SIMILARITY: BELONGS TO THE COMPLEX I 20 KDA SUBUNIT FAMILY.
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